

Fig. 1

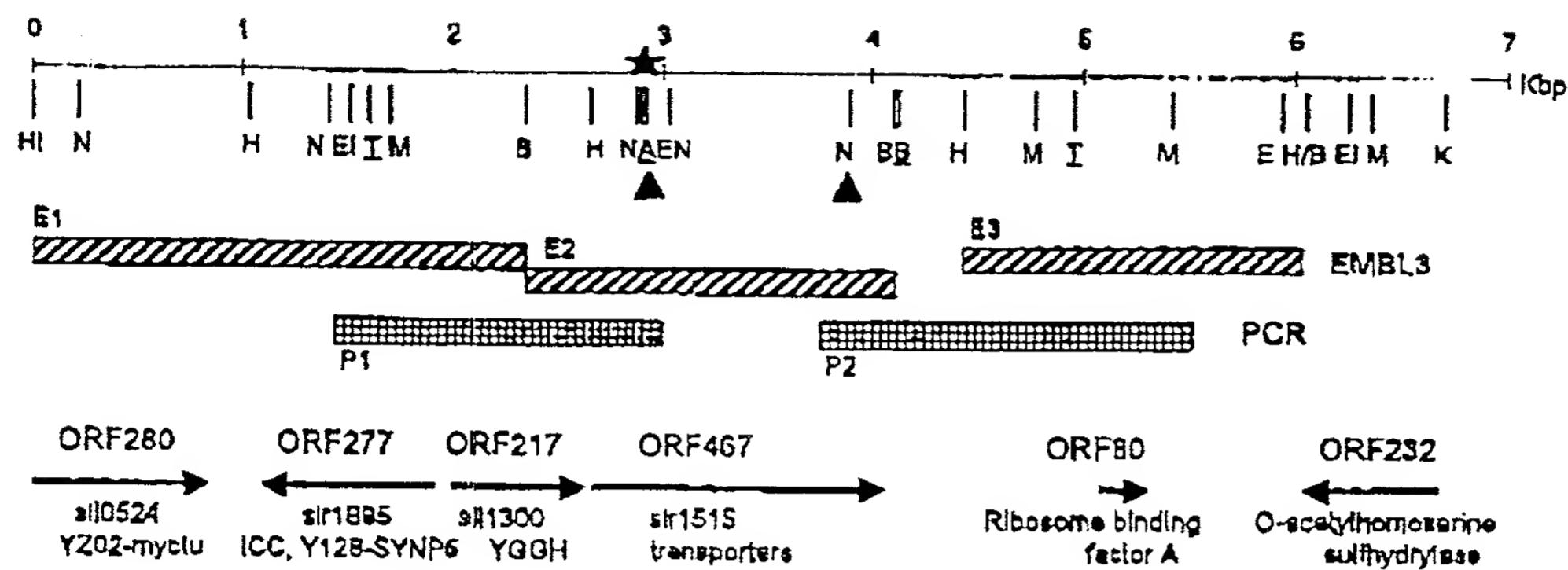


Fig. 4a

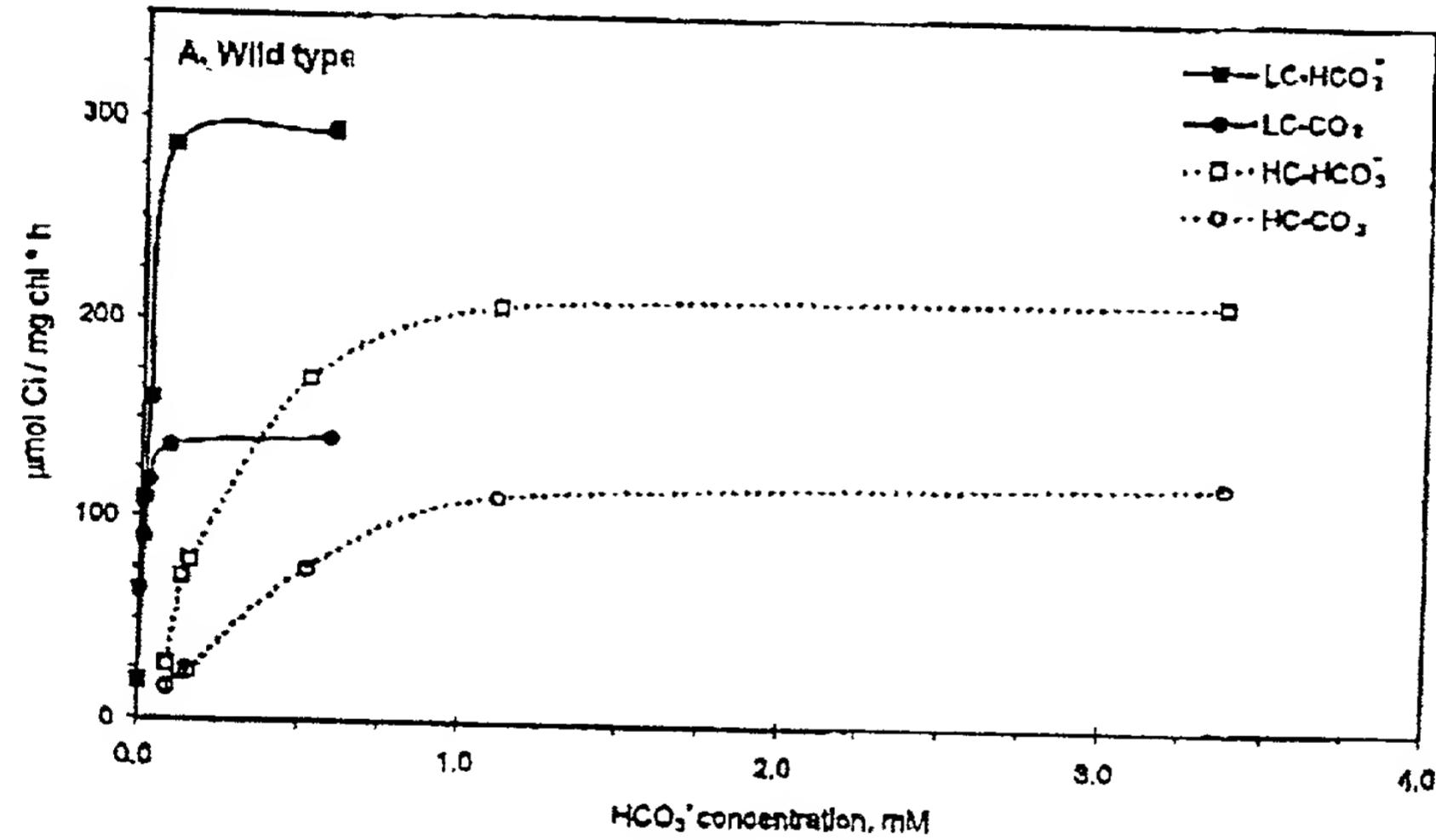


Fig. 4b

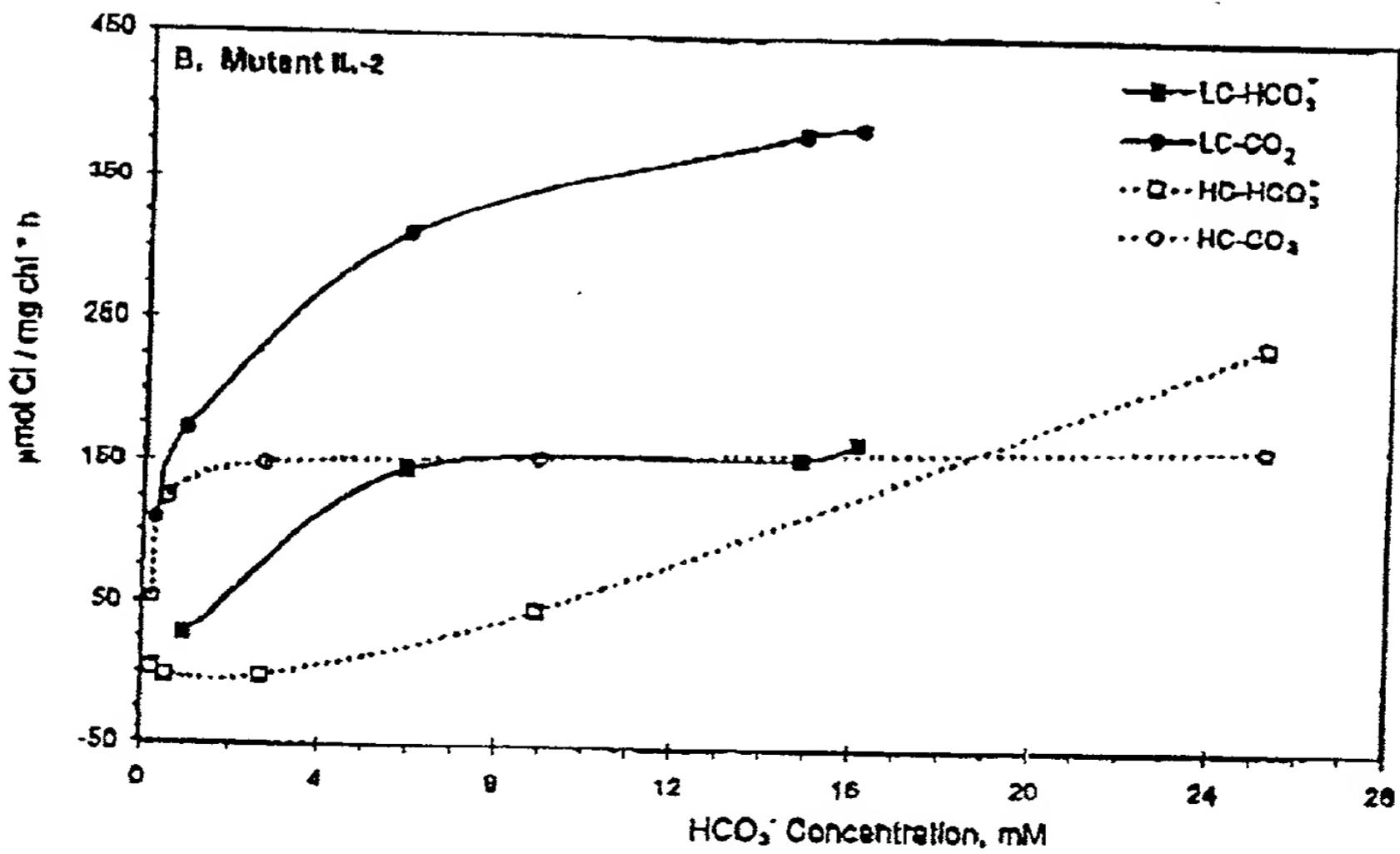


FIGURE 2

ICTB : 1 ATGACTGTCTGGCAAACCTCTGACTTTGCCATTACCAACCCAACAGTGGGCCACAGC 60 (SEQ ID NO:2)
||| ||| ||||| ||| ||||| ||||| ||| ||| ||| ||||| ||| |||
SLR : 13 ATCTCTATCTGGCGATCGCTGATGTTGGCGTTTCCCCCAGGAATGGGCCGGGC 72 (SEQ ID NO:4)

ICTB : 61 AGTTTCTTGCATCGGCTGTTGGCAGCCTGC-GAGCCTGGGGCCCTCCAGCCAGCTGTT 119
||| ||| ||||| ||| ||||| ||| ||||| ||| ||| ||| |||
SLR : 73 AGTGTGCTCCATCGTTGGTGGCTGGGACAGAG-TTGGATACAGGCTAGTGTGCTCTG 131

ICTB : 120 GGTTTGGTCTGAGGCACTGGGT--GGCTTCTTGCTGTCGTCTACGGTTGGCTCCG 177
| | | ||||| ||||| ||||| ||| ||| ||| ||| ||| ||| |||
SLR : 132 GCCCCACTTCGAGGCATTGGGTACGGCT-CTAG-TGGCAATAATTATTGGCGCTCCC 189

ICTB : 178 TTTGTGCCAGTTCCGCCCTAGGGTTGGGCTAGCCGCGATCGCG-GCCTATTGGGCCCT 236
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
SLR : 190 TTCACCTCCACCACCATGTTGGCATTGGTAT-GCTGCTCTGGAGCCTTGGCTCT 248

ICTB : 237 GCTCTCGCTGACAGATATCGATCTGGCAAGCA---ACCCCCATTCACTGGCTGGTGCT 293
||| | | | ||| | | | ||| | | | ||| ||| ||| | | | |
SLR : 249 GCTGACCTTGCTGAT--CAACCAG-GGAAGGGTTGACTCCCATCCATGTTTAGTTT 305

ICTB : 294 GCTCTACTGGGCGTCGATGCCCTAGCAACGGACTCTCACCCGTACGGCTGCAGCTT 353
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
SLR : 306 TGCCTACTGGTGCATTCGGCGATGCCGTGGGATTCTCCGGTAAAAATGGCGGCGGC 365

ICTB : 354 AGTTGGGCTAGCCAAACTGAC-GCTC-TACCTGTTGGTTTGCCTAGCGGCTCGGGTT 411
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
SLR : 366 GTCGGGGTTAGCGAAATTAAACAGCTAATTATGTTCTAC-TGGCGGCGAGGTTA 423

ICTB : 412 CTCCGCAATCCCCGTCTGC-GATCGCTGCTGTTCTCGGTGTCGTGATCACATCGCTTT 470
| | | | | | | | | | | | | | | | | | | | | | | | | |
SLR : 424 TTGCAAAACAAACAATGGTTAAC-CGGTTAGTAACCGTTGTTACTGGTAGGGCTATT 482

ICTB : 471 TGTCAGTGTCTACGGCCTCAACCAATGGATCTACGGCGTTGAAGAGCTGGCGACTGGGT 530
||| | | | ||| | | | | | | | | | | | | | | | | | | | |
SLR : 483 GGTGGGGAGTTACGGTCTGCGACAACAGGTGGACGGGTTAGAACAGTTAGCCACTGGAA 542

ICTB : 531 GGATCGCAAACCTGGTGGCGACTTCACCTCACGGTTACAGCTATCTGGCAACCCAA 590
||| | | | | | | | | | | | | | | | | | | | | | | | | |
SLR : 543 TGACCCCACCTCTACCTGGCCAGGCCACTAGGGTATATAGCTTTAGGTAAATCCCAA 602

ICTB : 591 CCTGCTGGCTGCTTATCTGGTGGCGACGACTGCCTTT-CTGCAGCAGCGATCGGGTGT 649
||| | | | | | | | | | | | | | | | | | | | | | | | | |
SLR : 603 TCTCTTGGCGGCTTACCTGGTGGCCATGACGGGTTGAGCTTGAGT-GCCCTGGTGGTAT 661

ICTB : 650 GGCGCGGCTGGCTCCCAAGCTGCTGGCGATCG-CTGCGACAGGTGGAGCAGCTTATGT 708
||| | | | | | | | | | | | | | | | | | | | | | | | | |
SLR : 662 GGCGACGGTGGTGGCCAAACTGCTGG-GAGCAACCAGGTGATTGTTAACCTACTCTGT 720

ICTB : 709 CTGATCCTCACCTACAGTCGCGGTGGCTGGCTGGTTTGTGCCATGATTTGTCTGG 768
||| | | | | | | | | | | | | | | | | | | | | | | | | |
SLR : 721 CTCTTTTTACCCAGAGCCGGGGCGGTGGCTAGCAGTGCTGGCCCTGGGAGCTACCTTC 780

ICTB : 769 GCGTTATTAGGGCTCTACTGGTTCAACCCCGTCTACCCGACCGCTGGCTGGCTA 828
| | | | | | | | | | | | | | | | | | | | | | | | | |
SLR : 781 CTGGCCCTTGTACTTCTGGTGGTTACCCAAATTACCCAAATTGGCAACGGTGGTCT 840

ICTB : 829 TTCCCAGTCGTATTGGGTGGACTAGTCGCGGTGCTCTT-GGTGGCGGTGCTGGACT--- 884
||| | | | | | | | | | | | | | | | | | | | | | | | | |
SLR : 841 TTGCCCCCTGGC---GATCGCC--GTGGCGGTATATTAGGTGGGGAGCGTTGATTGCG 894

ICTB : 885 -TG-AGCCGTTGCGCGTGCCTGGTGGAGCATCTTGTGGCGTGAAGACAGCAGCAAC 942
||| | | | | | | | | | | | | | | | | | | | | | | | | |
SLR : 895 GTGGAACCGATTGACTCAGGGCCATGAGCATTTGCTGGCGGAAAGACAGCAGTAAT 954

FIGURE 2 (CONTINUED)

ICTB :	943	AACTTCCGGATCAATGTCTGGCTGGCGGTGCTGCAGATGATTCAAGATCGGCCTGGCTG	1002
SLR :	955	AATTTCGGCATCAATGTTGGAAAGGGTAAAAGCCATGATCCGAGCCCCCTATCATT	1014
ICTB :	1003	GGCATCGGCCCGGCAATACCGCCTTAACCTGGTTATCCCTCTATCAACAGGCGCG	1062
SLR :	1015	GGCATTGGCCCAGGTAACGAAGCCTTAACCAAATTATCCTTACTATATGCGGCCCGC	1074
ICTB :	1063	TTTACGGCGTTGAGCGCCTACTCCGTCCCGCTGGAAGTCGCGGTTGAGGGCGGACTACTG	1122
SLR :	1075	TTCACCGCCCTGAGTGCCTATTCCATTACCTAGAAATTGGTGGAAACGGGTGTAGTT	1134
ICTB :	1123	GGCTTGA-CGGCCTTCGCTTGGCTGCT-GCTGGTCACGGCGGTGACGGCGGTGCGGCAGG	1180
SLR :	1135	GGTTTTACCTGTATGCTC-TGGCTGTTGGCCGTTACCCCTAGGCAAAGGC-GTAGAACTGG	1192
ICTB :	1181	TGAGCCGACTGCGGCGCGATCGCAATCCCC--AAGCCTTTGGTGATGGCTAGCTTGGC	1238
SLR :	1193	TTAAACG-CTGTCGC-CAAACCTCGCCCCGGAAGGCATCTGGATTATGGGGCTTAGC	1250
ICTB :	1239	CGGTTGGCAGGAATGCTGGTCACGGTCTGTTGATACCGTGCTATCGACCGGAAGC	1298
SLR :	1251	GGCGATCATCGGTTGTTGGTCCACGGCATGGTAGATACTGGATTACCGTCCCCCGGT	1310
ICTB :	1299	CAGTACGCTCTGGTGGCTCTGTATTGG--AGCGATCGCGAGTTCTGG--CAGC-CCCAA	1353
SLR :	1311	GAGCACTTGTGGTGG-TTGCTAGTGGCCATTG-TTGCTAGTCAGTGGGCCAGCGCCAG	1368
ICTB :	1354	CCTTCCAAGCAACTCCCTCCAGAAGCCGAGCATTAGACGAA	1395
SLR :	1369	GCCCGTTGGAGGCCAGTAAAGAA---GAAAATGAGGACAAA	1407

FIGURE 3

ICTB : 1 MTVWQTLTFAHYQPQQWGHSSFLHRLFGSLRAWRASSQLLVSEALGGFLLAVVYGSAPF 60
+++W++L F + PQ+WG S LHRL G ++W +S L EALG L+A+++ +APF
SLR : 5 ISIWRSLMFGGFSPQEWRGGSVLHRLVGQSWIQASVLWPHFEALGTALVIIIFIAAPF 64

ICTB : 61 VPSSALGLGLAAIAAYWALLSLTDIDLRQATPIHWLVLLYGVDALATGLSPVRAAALVG 120
++ LG+ + A+WALL+ D + TPIH LV YW + A+A G SPV+ AA G
SLR : 65 TSTTMLGIFMLLCGAFWALLTFADQPGKGLTPIHVLVFAYWCISIAVGFSVKMAASG 124

ICTB : 121 LAKLTLYLLVFAALARVLRNPRRLSLLFSVVVITSLFVSVYGLNQWIYGVVEELATWDRN 180
LAKLT L +F LAAR+L+N + + L +VV++ L V YGL Q + GVE+LATW D
SLR : 125 LAKLTANLCLFLAARLLQNKQWLNRVTVVLLVGLVGSYGLRQQVDGVEQLATWNDPT 184

ICTB : 181 SVADFTSRVSYLGNPNLLAAYLVPTTAFSAAAIGVWRGWLKPULLAIAATGASSLCLLT 240
S +RVYS+LGNPNLLAAYLVP T S +A+ VWR W PKLL + LCL T
SLR : 185 STLAQATRVYSFLGNPNLLAAYLVPMTGLSLSALVVWRRWPKLLGATMVIVNLLCLFFT 244

ICTB : 241 YSRGGWLGTVAMIFVWALLGLYWFQPRLPAPWRRWLFPVVLGLVAVLLVAVLGLPRLV 300
SRGGWL +A+ + L +W+ P+LP W+RW P+ + V + A++ +EP+R+
SLR : 245 QSRGGWLAVALGATFLALCYFWWLPQLPKFWQRWSLPLAIAAVAVILGGGALIAVEPIRL 304

ICTB : 301 RVLSIFVGREDSSNNFRINVWLAFLQMIQDRPWLGIQPGNTAFNLVYPLYQQARFTALSA 360
R +SIF GREDSSNNFRINVW V MI+ RP +GIGPGN AFN +YP Y + RFTALSA
SLR : 305 RAMSIFAGREDSSNNFRINVWEGVKAMIRARPIIGIGPGNEAFNQIYPPYYMRPRFTALSA 364

ICTB : 361 YSVPLEVAVEGGLLGLTAFAWLLVTAVTAVRQVSRLRRDRNPQAFWLMASLAGLAGMLG 420
YS+ LE+ VE G++G T WLL VT V V R R+ P+ W+M +LA + G+L
SLR : 365 YSIYLEILVETGVVGFTCMLWLLAVTLGKVELVKRCRQTLAPEGIWIMGALAAIIGLLV 424

ICTB : 421 HGLFDTVLYRPEASTLWWLCIGAIASFQWQPQPSKQLPPEAEHSDEKM 467
HG+ DTV YRP STLWWL + +AS W ++ + E+ D+ +
SLR : 425 HGMVDTVWYRPPVSTLWWLLVAIVASQWASAQARLEASKEENEDKPL 471

Fig. 5

Wild type GGGCT-AGCCGGCATCGCGGCCTATTGGGCC (SEQ ID NO:6)
IL-2 ApaI side GGGCT-AG--G-GATCGC-GCCTATTGGGCC (SEQ ID NO:7)
IL-2 BamHI side GGGCTCA-----GATCGC-GCCTATTGGGCC (SEQ ID NO:8)
IctB G L A A I A A Y W A L (SEQ ID NO:9)

Fig. 6

